

- (a) obtaining a sample of pig nucleic acid; and
- (b) analysing the nucleic acid obtained in (a) to determine whether a mutation is/is not present at an exon 17/intron 17 splice site of a KIT gene, wherein the mutation consists of the substitution of the G in the conserved GT pair by A.--

Please rewrite claim 10 to recite the following:

--10 (Twice Amended). The method according to claim 8, wherein the ratio of restriction fragment lengths is determined.--

Please rewrite claim 14 to recite the following:

--14. (Thrice amended). A method for determining coat colour genotype in a pig which comprises the step of analysing a sample of pig KIT protein to determine whether the protein is a splice variant protein produced by the substitution of G in the conserved GT pair by A, at an exon 17/intron 17 splice site of a KIT gene, said splice variant protein being correlated with coat colour genotype.--

Please rewrite claim 15 to recite the following:

--15. (Thrice amended). A kit for use in determining the coat colour genotype of a pig which comprises one or more reagents for carrying out PCR and the following pair of primers:

5'-GTA TTC ACA GAG ACT TGG CGG C-3' (SEQ ID NO:1);
5'-AAA CCT GCA AGG AAA ATC CTT CAC GG-3' (SEQ ID NO:2).--

Please cancel claims 3, 16 and 17 without prejudice or disclaimer.

Please add the following new claims 18 and 19 as set forth below:

--18 (new) The method of claim 1, wherein the presence or absence of said mutation is determined in each copy of the KIT gene in the pig's genome, and the ratio of the number of KIT genes lacking the mutation to the number of KIT genes containing the mutation is determined.--

--19. (new) The method according to claim 9, wherein the ratio of restriction fragment lengths is determined.--